PATENT
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METHODS FOR DETERMINING THE BIOCHEMICAL AND BIOPHYSICAL PROPERTIES OF PROTEINS

FIELD OF THE INVENTION

The present invention relates to a method of determining the biochemical or biophysical properties of a protein from its amino acid sequence. The invention further relates to a method for optimizing high-throughput protein expression and protein structure determination. Additionally, the present invention relates to a method for optimizing the screening of proteins as potential drug-targets and optimizing drug discovery techniques.

BACKGROUND OF THE INVENTION

Genome sequencing projects are providing vast amounts of information. With the whole genome of many organisms, including humans, complete or nearing completion, the next challenge involves the characterization of these gene products, proteins. The characterization of proteins has focused on both the analysis of the 3-dimensional structure and of the corresponding function.

The completion and near completion of the sequencing phase of genome projects has ushered in the age of proteomics, the study of all gene products in an organism. This flood of sequence information coupled with recent advances in molecular and structural biology have also lead to the concept of "structural proteomics" or "structural genomics", the determination of 3-dimensional protein structures on a genome-wide scale. An important use of 3D-structural information of proteins is to uncover clues to protein function that are not detectable from sequence analysis. This application of structural proteomics is driven by the realization that fewer than 30% of all predicted eukaryotic proteins have a known function.

While useful, analysis of the DNA sequence alone, generally does not allow one to infer the structure or function of gene products unless the sequence has high homology to another gene of known function. Gene sequence information does not provide a complete and accurate profile of protein function or structure. After transcription from DNA to RNA, the mRNA transcript may be spliced in different ways prior to translation into the protein. Following translation, many proteins are modified, for example by the addition of one or more carbohydrate or phosphate groups. These modifications are important to the structure and function of the protein but are not directly coded by that protein's gene. Thus, a single gene can code for many protein products. As a consequence, the proteome is far more complex than the genome.

The function of a protein derives from its 3-dimensional structure. The sequence information alone is generally insufficient to provide a detailed picture of a protein's structure and function. The 3-dimensional structure of a protein generally provides more information about function than does the sequence of the protein. Proteins with little sequence homology but high structural homology have often been found to have similar biochemical functions. The function of a protein often involves interaction with a small molecule, another protein or other biomolecule, such as a lipid, sugar, or nucleic acid. The interaction of the protein with its target molecule is determined by amino acid residues which are close in space due to the protein's 3-dimensional structure, allowing those residues to simultaneously interact with the target molecule. However, these amino acids may be distant according to the linear amino acid sequence.

To predict a function for a new protein, the amino acid sequence of the predicted protein coding region, or open reading frame (ORF), is compared against all functionally assigned sequences in protein sequence databases. If significant sequence or motif homology is found between the ORF and a sequence of known function from the protein sequence database, it is assumed that the two sequences share the same, or similar, function. Unfortunately, most ORFs share little or no or only partial homology with a functionally assigned sequence. Thus, a large proportion of new ORFs are found to encode proteins of unknown function. In addition, for those ORFs that harbor some homology to another sequence, often the region of homology comprises only a small fraction of the total sequence, leaving the rest unknown.

The function of a new protein can often be predicted by determining its 3-dimensional structure using nuclear magnetic resonance (NMR) or X-ray crystallography. The structure, rather than the amino acid sequence, is then compared to known protein structures of assigned function. This information is collected in the Protein Data Bank (PDB), which can be searched to find homologous structural features of known proteins. If structural homologs are found, the new protein may be predicted to have a function similar to that of the homolog. In many cases confirmation of the predicted function can be readily determined experimentally. This method has the potential to be far more reliable than primary sequence comparisons, as proteins with little sequence homology may adopt similar 3-dimensional conformations that impart similar function. However, to date the PDB database contains relatively few unique protein structures (<2000) giving the database limited predictive powers.

A related use of structural proteomics information is to determine a sufficient number of three-dimensional structures necessary to define a "basic parts list" of protein folds. Most other structures could then be modeled from this basis-set using computational techniques. This analysis becomes feasible when a sufficient number of high-resolution, three-dimensional protein structures have been determined to establish rules of how all proteins fold into functional biological macromolecules. The long term goal is to determine experimental structures for all proteins because it is the subtle *differences* in protein structure that contribute to the diversity and complexity of life, and current modeling techniques are not yet accurate enough to reveal these subtleties.

As protein structure is fundamental to molecular biology and disease, structural proteomics will have an impact impacts on many areas of biology including drug development. Application of structural proteomics to the pharmaceutical industry includes providing protein structural information for drug development, including identification and/or validation of new drug targets.

Historically, the explosion in gene sequence information has far outpaced the characterization of gene products. The processes of expressing and purifying proteins have represented a bottleneck in the efforts to obtain protein samples for 3-dimensional structure

determination by NMR and X-ray crystallography. Current methods to express and purify proteins for structural determination are performed on a protein-by-protein basis with relatively low throughput. Generating high quality samples for structure determination by NMR or by X-ray crystallography (a well-behaving NMR sample or a well-diffracting crystal, respectively), is also a bottleneck in these efforts. An essential element for the success of structural proteomics is the development of high-throughput methods for protein expression, purification, sample preparation and structural determination.

The invention provides for a database of protein sequence information and experimentally determined biochemical and biophysical properties of proteins. The database is analyzed using data-mining techniques to find correlations among protein sequence information, biochemical properties and biophysical properties. The correlations provide predictive rules relating a protein's sequence to its biochemical and biophysical behavior. Using the correlations obtained from the data-mining techniques, the properties of new proteins are determined given their amino acid sequence information. This allows the optimization of the conditions necessary for high-throughput techniques, such as expression, purification, crystallization, NMR-sample preparation, structure determination and screening for binding to other molecules. The high-throughput analysis of protein structure is intrinsic to the success of structural proteomics. Such high-throughput analysis is also applied to techniques for screening proteins as potential drug-targets. The predictive rules are useful for the optimization of conditions for drug discovery, greatly accelerating rational drug development.

SUMMARY OF THE INVENTION

It is an object of this invention to provide a general strategy for determining relationships among a protein's biochemical properties, biophysical properties and sequence. With the extraordinary volume of gene sequence information identified by the genome projects, the volume of protein sequence information will increase rapidly.

It is an object of this invention to provide a database of protein sequence information and experimentally determined protein properties. The database can be analyzed using data-mining

techniques to find correlations among protein sequence information, biochemical properties and biophysical properties. Using the empirical correlations obtained from the data-mining techniques, the properties of new proteins are determined given their amino acid sequence information alone or using a combination of the sequence information and one or more properties.

Another object of the invention is to provide a method of determining the properties of a protein using the sequence information alone or in combination with one or more properties by applying the correlations obtained by the analysis of this database.

A further object of the invention is to provide a method for optimizing high-throughput protein structure determination. Using the predictive power of the empirical database in conjunction with data-mining tools, and the correlations obtained therefrom, the biochemical and biophysical properties of new proteins can be predicted. Based upon these predictions, experimental conditions for the analysis of a protein, or class of proteins, are modified so that the analysis can be better performed. Conversely, the invention provides a screening method to identify proteins that exhibit the desired properties for structural analysis by NMR or X-ray crystallography.

A further object of the invention is to provide a method for optimizing high-throughput methods for drug-target discovery. The invention provides a method of predicting which proteins are amenable to investigation as drug targets, thus speeding up the drug discovery process. The invention provides a screening method to identify proteins that exhibit the desired properties for study as potential drug targets.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. is a decision tree for discriminating between soluble and insoluble proteins. The nodes of the tree are represented by ellipses (intermediate nodes) and rectangles (final nodes or leaves).

DETAILED DESCRIPTION

We have found that given a database of protein sequence and experimentally determined protein properties, we are able to derive a set of rules from protein sequence information that are predictive of a given protein's biophysical and biochemical properties. The proteins may include naturally occurring proteins, modified proteins, synthetic proteins and subdomains of proteins. It is often easier to work with the smaller subdomain of a given protein, for example in drug screening or drug design, and also structure determination.

The database is constructed from protein sequence information and experimental data on protein biophysical and biochemical properties. The protein sequence information includes the primary amino acid sequence and characteristics which are directly derived from the sequence, including amino acid composition, the character of a region of the sequence, hydrophobicity, charge, molecular weight, the presence and length of low complexity regions and the presence of sequence motifs found in other proteins. The amino acid composition includes such information as the percent of a specific amino acid present in the sequence, the percent of a combination of two or more amino acids, and the percent of amino acids of a general class (such as, but not limited to, hydrophobic, hydrophillic, aromatic, aliphatic, acidic, basic, charged, and the like). Regions having a particular character may be, for example, regions of low sequence complexity, regions that are hydrophobic/hydrophilic, or charged regions (positive or negative). The source or the sequence information is derived from the genomic DNA sequence, cDNA sequence, or synthetic DNA. The primary sequence information may come from any source, including human, animals, plants, yeast, bacteria, virus or engineered proteins.

The biophysical properties which populate the database include, for example, thermal stability, solubility, isoelectric point, pH stability, crystalizability, conditions of crystallization, aggregation state, heat capacity (ΔC_p), resistance to chemical denaturation, resistance to proteolytic degradation, amide hydrogen exchange data, behavior on chromatographic matrices, electrophoretic mobility and resistance to degradation during mass spectrometry. Biophysical properties may also include amenability (suitability) for study by various investigative techniques, including nuclear magnetic resonance (NMR), X-ray crystallography, circular

dichroism (CD), light scattering, atomic adsorption, fluorescence, fluorescence quenching, mass spectroscopy, infrared spectroscopy (IR), electron microscopy, atomic force microscopy and any results obtained from these techniques. For each property, the conditions under which the property was determined is incorporated into the database. These conditions may include solvent choice, protein concentration, buffer components and concentration, pH, temperature and salt concentration. It is advantageous to record a protein's properties determined under a variety of experimental conditions. Additional proteins are studied using the same set of conditions. In all cases where it is applicable, negative information is recorded in the database (for example, insolubility, unsuitability for study by NMR, etc.) To insure uniformity of the data collected, it is preferred to perform the biophysical measurements on proteins that have been purified. It is especially preferable that the proteins are at least about 95% pure.

Among the biophysical properties which may be included in the database are those that relate to X-ray crystallographic techniques. These properties include conditions under which a protein does or does not crystallize, including solvents, precipitants, buffer components and concentration, pH, temperature, and salt concentration. The properties also include any results obtained from the X-ray crystallography studies, including three dimensional structure, characteristics of the crystal, including space group, solvent content, unit cell parameters, crystal contacts, solution conditions and bound water, and substrate binding. Additionally, the database may include how the various conditions employed effect result that are obtained.

The biochemical properties which compose the database include expressability, or level of expression, in various vectors and hosts with various fusion tags and under various conditions, such as temperature and medium composition, the protein yield obtained from various vectors and hosts under various conditions, results of small molecule binding screens, subcellular localization, demonstrated utility as a drug target, and knowledge of protein-protein or protein-ligand interactions. A biochemical property of particular interest is the protein's potential as a drug target.

An important aspect of the method of the invention is to have large numbers of proteins examined and compared under uniform conditions. The advent of high-throughput cloning and

expression techniques and of high-throughput protein purification techniques has contributed to the feasibility of collecting this large volume of information. In theory, one might be able to compile the type of data listed above on a larger number of proteins from published accounts in the literature. Data from literature sources is not acquired under "standard" or uniform conditions. Furthermore, it is hard to assess the quality control or to fully ascertain the experimental conditions in many literature papers. Therefore, such a literature database would inherently yield less reliable predictions. For example, one can find data on protein yields from *E.coli* expression for many proteins. However, the conditions of growth (length of incubation time, temperature, induction conditions... etc) are variable and can have effects on the experimental result. Thus, correlations between protein characteristics and expressability based on such data would be unreliable. Additionally, the intrinsic noise or scatter in the data will mask more subtle correlations. Furthermore, negative results are not reported in the literature, and these are just as important to record in the database and use in the data mining (for example: under what conditions is a given protein not soluble, or does a given protein not crystallize).

According to the invention, to insure uniformity of the data, the biophysical and biochemical data are collected using a uniform set of conditions or experimental procedures. The conditions under which the empirical data are collected are important and are recorded in the database. Ideally, multiple conditions are recorded for each type of measurement. The conditions of the data collection (temperature, solution components, salt concentration, buffer, pH) can drastically effect the behavior of a given protein. Therefore, it is desirable to compare many proteins under the same set of conditions, so that the only variable is the protein sequence. Alternatively, one can compare a variety of conditions for a give protein (or set of proteins) and relate that to sequence features.

In order to mine this data, it is annotated in the database using a "controlled vocabulary". For example, data entry for solubility could be either a number, such as a quantitative measurement (for example, solubility in mg/ml), or a qualitative numerical scale (for example, a scale of 0-5, with 0 being completely insoluble, and 5 being very soluble). Direct instrumental measurements can also be used if internal calibration standards are used, so that the values can be related to some standard.

As a sufficient quantity of data is compiled in the database, the data can be analyzed using data-mining techniques, or knowledge discovery tools, to find correlations among protein sequence information and biochemical or biophysical properties. These correlations provide predictive rules for general protein behavior. The correlations may link protein sequence information alone, or in combination with one or more biochemical or biophysical properties, to a certain characteristic or a set of characteristics. Using the correlations obtained from the data-mining techniques, the properties of new proteins are determined given their amino acid sequence information alone or using a combination of the sequence information and one or more empirical properties.

Data-mining techniques, or knowledge discovery tools, are computer algorithms and associated software for identifying relationships between elements of the database, particularly relationships to protein sequence features. Data-mining techniques include, for example, decision-tree analysis, case-based reasoning, Bayesian classifier, simple linear discriminant analysis, and support vector machines. We found decision tree analysis to be most useful for comprehensibly summarizing the multivariate data and for developing prediction rules of a relatively small database of protein solubility and crystallization data .

The predictive nature of the invention allows one to preemptively adjust experimental conditions to optimize, for example, cloning techniques, protein expression techniques, purification techniques and protein structure determination techniques. Thus, the invention provides a method for optimizing high-throughput protein structure determination. Using the predictive power of the empirical database in conjunction with data-mining tools, and the correlations obtained therefrom, the biochemical and biophysical properties of new proteins are predicted. Based upon these predictions, experimental conditions for the analysis of a protein, or class of proteins, is modified. Conversely, the invention provides a screening method to identify proteins that exhibit the desired properties for structural analysis or for use as a substrate for high-throughput drug screening. By the method of the invention, the biochemical or biophysical properties of new proteins are determined. Proteins that are determined to have a desired property or properties are then selected for further analysis. In this way, optimal proteins can be selected based on properties including one or more of crystallizability, suitability for NMR,

expressability in a certain vector, solubility, suitability for study by a certain investigative technique and suitability for drug screens.

The method of the invention speeds up the high-throughput structure determination process. The three dimensional structure of a protein can reveal whether it is likely to be a good drug target. Good drug targets generally, have deep, often hydrophobic, clefts or grooves on their surface or at their active sites where small molecule drugs can bind with high affinity. Poor drug targets have shallow grooves or otherwise poor surface properties that do not allow for high affinity binding of small molecules. By rapidly identifying which proteins have surface properties that make it promising for drug binding, the method greatly facilitates the drug discovery process.

The invention provides a method to identify proteins that exhibit desired biochemical properties for drug interaction. Such biochemical properties may include the propensity to bind or interact with certain small molecules such as, for example, hydrophobic compounds, carbohydrates, or metal ions, or certain classes of drugs, pesticides, herbicide, or insecticides. By the method of the invention, the properties of new proteins are determined. Proteins that are determined to have a desired property or properties are then selected for further analysis. The screening of proteins as potential drug targets allows the researcher to selectively study proteins that are predicted to have desired biochemical or biophysical properties, thus reducing the research time and costs while greatly increasing the chance of success. The invention provides a method of predicting which proteins are amenable to investigation as drug targets, thus speeding up the drug discovery process.

For example, using the method of the invention, allows us to predict from protein sequence information which proteins will be soluble and stable - a requirement for high-throughput screening of drug-target candidates. Thus, it greatly facilitates the development of high-throughput screening methods. Additionally, it will allow us to predict which proteins will crystalize, and under what conditions, and which proteins will be amenable to NMR structure determination. The structure of a protein is useful in designing inhibitors or drugs that target that protein. The invention provides a rapid method of predicting which proteins are amenable to

structure determination, thus speeding up the drug discovery process. In addition, the method of the invention will tell us which sequence features make a protein less amenable to structure determination, or less soluble and less stable. Thus, it provides the necessary knowledge to make point mutations, allowing the production of an analogous protein that will be more amenable to structure determination, or more soluble and more stable, again facilitating the target identification, validation and high-throughput screening and drug design processes. Certain classes of proteins, such as a specific enzyme class, may exhibit unique biochemical or biophysical properties. The invention would allow the creation of "class-specific" characteristics, which would allow us to discover new members of the class or to modify members of the class to be more optimal in terms of activity, solubility or suitability for structure determination.

The more protein and characteristics compiled in the database, the greater the predictive powers achieved from the rules derived from the data-mining. For this reason the use of high throughput techniques in the assembly of the database is desirable. The wide availability of recombinant DNA technology makes it feasible to generate expression systems that can produce large quantities of a selected protein. The steps for protein production may include: generation of the protein expression systems, overexpressing the protein and purifying the protein.

The generation of a clone for any particular gene of interest, and its incorporation into a suitable expression vector, is now a straightforward task that can be done in a parallel fashion for high-throughput production. The selection of target proteins for structural analysis from completely sequenced genomes can take advantage of the availability of these cloned genes. However, even if a clone of a particular protein of interest is not readily available, it has now become a routine operation to generate a cDNA clone for almost any particular protein from a wide variety of organisms.

To obtain expression of a cloned nucleic acid, the expression vector for expression in bacteria contains a strong promoter to direct transcription, a transcription/translation terminator, and if the nucleic acid encodes a peptide or polypeptide, a ribosome binding site for translational initiation. Suitable bacterial promoters are well known in the art and described, e.g., in

Sambrook et al. and Ausubel et al. Bacterial expression systems are available in, e.g., E. coli, Bacillus sp., and Salmonella (Palva et al., Gene 22:229-235 (1983); Mosbach et al., Nature 302:543-545 (1983). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are well known in the art and are also commercially available. In certain cases, where post-translational modifications, for example, glycosylation are important, eukaryotic expression systems are preferred. In some cases, it may be preferable to employ expression vectors which can be propagated in both prokaryotic and eukaryotic cells, enabling, for example, nucleic acid purification and analysis using one organism and protein expression using another.

Transfection methods used to produce bacterial, mammalian, yeast or insect cells or cell lines that express large quantities of protein are well known in the art. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g., Sambrook et al., supra). After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of protein, which are then purified using standard techniques.

The protein is expressed in suitable amounts for further analysis. There are several expression systems that have been extensively studied. Some of these include: 1) bacterial (*E. coli*), 2) methylotrophic yeast (*Pichia pastorisis*), 3) viral (baculovirus, adenovirus, vaccinia and some RNA viruses), 4) cell culture (mammalian and insect), and 5) *in vitro* translation. Although the expression of any particular protein may be idiosyncratic, the availability of these and other expression systems significantly increases the ability to produce large quantities of protein.

In situations in which relatively large amounts of relatively pure protein in native form are required, for example to obtain protein crystals useful for determination of 3D structure, it will be desirable to employ expression systems characterized by high expression levels, efficient protein processing including cleavage of signal peptides and other post-translational modifications. The baculovirus expression system is widely used to express a variety of proteins

in large quantities. In addition to fulfilling the above requirements, the size of the expressed protein is not limited, and expressed proteins are typically correctly folded and in a biologically active state. Baclovirus expression vectors and expression systems are commercially available (Clontech, Palo Alto, CA; Invitrogen Corp., Carlsbad, CA).

Once a protein has been expressed to an acceptable level, the protein is purified from the other contents of the cell system that was utilized for expression. Highly purified protein is often desirable for further analysis according to the method of the invention. The proteins can be expressed fused to tags that aid subsequent purification or measurement techniques. Typical tags bind specifically to particular ligands, allowing the attached protein to be purified without regard to its physical or biochemical characteristics. Such tags can then be cleaved, leaving the protein in its native form. Examples of tags include histidine rich sequences which bind to various metal ions and glutathione-S-transferase (GST) tags which selectively bind to glutathione. The ligands are typically attached to a solid support. The fusion proteins are bound to the immobilized ligand and unbound material is removed. In certain cases, the fusion protein also includes a cleavable sequence of amino acids between the protein of interest and the tag sequence whereby the tag can be cleaved from the protein of interest. Typically, this is accomplished with a protease that cleaves the sequence under conditions where the protein of interest is not degraded, or with an intein sequence, which allows for internal cleavage of the protein. Alternatively, the tags can provide a method for specifically anchoring proteins to a solid support for assay purposes. For example, it can be useful to anchor proteins to an assay plate in order to measure fluorescence and fluorescence quenching in the presence of potential ligands. In another embodiment, a solid support is employed which provides an array of binding surfaces to which different proteins of the library are anchored for use in protein-ligand and protein-protein interaction studies. The solid support can be, for example, a glass or plastic plate, a semi-solid or gel-like matrix or the surface of a semiconductor measuring device. Bacterial vectors designed for production of GST fusion proteins are commercially available which allow cloning of DNAs in all three reading frames (e.g., pGEX series of vectors; Amersham Pharmacia Biotech, Inc., Piscataway, NJ).

The following examples are provided as illustrative of the present invention and are not limiting.

EXAMPLE I

To explore the feasibility of a comprehensive structural proteomics project, 424 non-membrane proteins of unknown structure from *Methanobacterium thermoautotrophicum* are cloned, expressed in *E. coli* and purified. Using a single high-throughput protocol, about 20% of these are found to be suitable candidates for x-ray crystallographic or NMR spectroscopic analysis without further optimization of conditions, providing an estimate of the number of the most readily accessible structural targets in a proteome. A retrospective analysis of the empirical characteristics, including the experimental behavior, of these proteins provides some simple relations between sequence and biochemical and biophysical properties. A comprehensive database of protein properties is useful in optimizing high-throughput strategies.

Target selection

M.th. is a thermophilic Archaeon whose genome comprises 1871 Open Reading Frames[7]. Archaeal proteins share many sequence and functional features with eukaryotic proteins, but are often smaller and more robust, and thus serve as excellent model systems for complex processes. Only two exclusionary criteria are implemented in our target selection scheme. First, membrane-associated proteins, which comprise approximately 30% (267-422 of 1871 ORFs) of the *M.th.* proteome, are excluded. Second, proteins that have clear homologues in the PDB are excluded (approximately 27% of *M.th.* proteins). The remaining proteins (~900) are not prioritized based on their probability of having a new fold, nor in terms of "biological relevance". We chose to invest our effort in developing high-throughput methods to generate a large collection of proteins to test as candidates for structural analysis, rather than concentrating on a small set of "high priority" targets, a large proportion of which may not be amenable for immediate structural analysis. Thus, 424 of the 900 final target *M.th.* proteins (almost a quarter of the entire proteome and a third of the non-membrane proteins) are chosen for cloning, expression and subsequent studies. These represent an unbiased sampling of non-membrane proteins from a single proteome with 34% having a functional annotation, 54% classified as "conserved" and 12% as "unknown". This diverse collection of proteins is particularly valuable for retrospective analysis aimed at identifying sequence features that are predictive of protein biophysical and biochemical behavior.

Cloning strategy

Each target gene is PCR-amplified from genomic DNA under standard, but optimized, conditions, with terminal incorporation of unique restriction sites, using high fidelity *Pfu* DNA polymerase (Stratagene). The PCR products are directionally cloned into the pET15b bacterial expression vector (NOVAGEN). The resulting plasmid encodes a fusion protein with an N-terminal hexa-histidine tag followed by a thrombin cleavage site. In the interest of throughput, no other expression vectors or organisms were used.

A single PCR protocol and set of cloning conditions are optimized for *M.th.* based on an analysis of an initial set of 50 genes. Positive clones are confirmed by colony PCR screening using Taq DNA polymerase. The generic nature of the procedure resulted in some PCR and sub-cloning failures, leading to a cumulative attrition rate of ~6%. This protocol is readily scalable to 96-well format and has been extended to alternative vectors and expression organisms.

Expression strategy

The *M.th.* open reading frames are divided arbitrarily into two groups, "large" (>20 kDa monomer size) and "small" (<20 kDa). Large proteins are processed for crystallization trials and small proteins for NMR feasibility studies. Most (~80%) successfully cloned *M.th.* proteins could be expressed in *E coli* BL21 -Gold (DE3) cells (Stratagene), although efficient expression often requires the presence of a second plasmid encoding three tRNAs which are frequently used by archeons and eukaryotes but are rare in *E. coli*. While most proteins are expressed to reasonable levels, many are not expressed in soluble form (<0.5 mg/L soluble protein), especially in the case of the larger proteins. It is possible to reduce the attrition rate due to poor solubility by optimizing the expression conditions for each clone. However, in the interest of throughput we used a single set of growth conditions optimized for the majority of proteins.

Purification and crystallization of large proteins

For large proteins, three colonies from each transformation are tested for protein expression on a small scale (50 mL). Proteins found to be soluble by SDS-PAGE analysis of the bacterial extract are prepared on a larger scale (2 L). These proteins are purified by a combination of heat-treatment (55°C) and nickel affinity chromatography, followed by thrombin cleavage and removal of the hexa-histidine tag. The heat treatment causes a significant

enrichment of many, but not all, *M.th.* proteins. The purification of the proteins is monitored by denaturing gel electrophoresis and occasionally by mass spectrometry. Proteins that survive the purification process (~75%) are concentrated to 10 mg/ml and subjected to a sparse-matrix crystallization screen of 48 conditions at room temperature (Matrix screen 1; Hampton Research). For each protein that crystallizes in the initial screen, conditions are further optimized using an expansion of related solution conditions (typically 18-20 screens of 24 conditions for each protein). We chose 24 of the proteins that formed crystals in the primary screen to follow up with optimization screens. Of these 11 formed well diffracting crystals (< 3.0 A). The implementation of automated methods for setting up and monitoring crystal screens can improve the throughput this process.

Purification and NMR screening of small proteins

The smaller proteins (<20 kDa predicted monomer size) destined for NMR analysis are expressed five at a time, each in 1L of ^{15}N-enriched minimal media and purified in parallel using metal affinity chromatography. The resulting ^{15}N-labeled hexa-histidine fusion proteins are concentrated by ultrafiltration to ~ 5-20 mg/ml, and the ^{15}N-HSQC NMR spectrum taken at 25°C. The HSQC spectra are classified into one of three categories. The first, termed "excellent" and indicative of soluble, globular proteins, contained the predicted number of dispersed peaks of roughly equal intensity. These excellent spectra suggest that the process of determining their 3D structure is relatively straight- forward. The second type of spectrum, termed "promising", had features such as too few or too many peaks and/or broad but dispersed signals. This suggests that optimization of either the protein construct or the solution conditions would be needed to yield an excellent sample. The last category, termed "poor", comprises two kinds of spectra. The first, which have intense peaks but with little dispersion in the ^{15}N-dimension, most likely reflects proteins that are soluble yet, largely unfolded. The second class has very low signal-to-noise and/or a single cluster of very broad peaks in the center of the spectrum. This class probably represents proteins which aggregate nonspecifically at concentrations required for NMR spectroscopy and thus are not readily amenable to structural analysis. For the 100 soluble proteins tested, the ratio of excellent/promising/poor spectra was 33/10/57.

Of the 33 proteins showing excellent spectra, seven are initially chosen for more detailed

structure determination using NMR spectroscopy. For these samples the his-affinity tag is removed by proteolytic cleavage; this does not markedly change the spectral properties of the proteins, suggesting that this step may be omitted in the interest of saving time and maximizing protein yield. In one case (MTH40) it was necessary to further optimize solution conditions in order to prepare a sample that was stable for the time period (several weeks) necessary for NMR data collection.

EXAMPLE II

Analysis of Protein Folding and Stability by Circular Dichroism (CD) Spectroscopy:

To explore how other spectroscopic techniques might aid in the identification of proteins suitable for detailed structural analysis, CD experiments are performed on 100 of the small, soluble MT proteins. Of the 28 proteins with excellent NMR spectra that are examined, all but 6 displayed CD spectra that were typical of folded proteins containing a significant fraction of α-helical and/or β-sheet secondary structure. The six atypical spectra may have resulted from unusual structural features of the proteins in question (e.g. small β-sheet proteins like SH3 domains possess very unusual CD spectra). Interestingly, 24 out of 32 proteins classified as "aggregated" by NMR spectroscopy display CD spectra consistent with stable, folded proteins. This suggests that the aggregation mechanism for many of the NMR samples may be due to surface interactions in the folded state, as opposed to aggregation of the exposed hydrophobic cores of unfolded proteins. Knowledge of the aggregation mechanism is useful for optimizing solution conditions that disfavor aggregation and therefore, CD provides a useful secondary screen in structural proteomics projects.

To better understand the contribution of protein stability to sample behavior, the thermal unfolding of 60 folded MT proteins is analyzed. Of these, 22 are unfolded and refolded in a fully reversible manner. However, among the 19 proteins with "excellent" NMR spectra that are tested in this manner, only 9 refold reversibly. The others precipitate at high temperatures, demonstrating that even among well-folded, small, soluble proteins, reversible thermal unfolding *in vitro* is not a ubiquitous property. Surprisingly, 8 proteins classified as "aggregated" by NMR are well-behaved in thermal unfolding experiments, indicating that these proteins are probably large discrete oligomers rather than non-specific aggregates.

As expected for proteins from a thermophilic organism, those from *M.th.* all possess high thermostability with transition midpoint temperature (T_m) values between 68°C and 98°C. Due to their low change in heat capacity (ΔC_p) upon unfolding, small proteins are generally expected to have higher T_m values compared to larger proteins [8]. Here, however, we observe no correlation between the length of the MT proteins and their T^m values. The ΔC_p values of small *M.th.* proteins are within the expected range as compared to a large number of other proteins that have been investigated (data not shown; [9]). These data suggest that except for their high thermal stability, the overall thermodynamic behavior of *M.th.* proteins studied here may be representative of other mesophilic organisms.

EXAMPLE III

Retrospective analysis of a database of biophysical and/or biochemical properties

These studies reveal that poor expression and solubility account for almost 60% of the recalcitrant proteins. To identify the parameters that contribute to this poor sample behavior (and other factors related to suitability for expression, purification, and structure analysis), a retrospective data-mining approach is applied. Sequence data from the ~424 proteins and the biophysical and biochemical data (expressability, crystallizability, solubility and melting temperature) are used to compile a database. Decision trees are useful for comprehensibly summarizing multivariate data and developing simple prediction rules. Growing the trees requires devising strategies regarding which variables (or combination of variables) to divide on, and what threshold to use to achieve the split. The 53 "splitting variables" used are derived from simple attributes of each sequence (e.g. amino acid composition, similarity to other proteins, measures of hydrophobicity, regions of low sequence complexity, etc.).

The full tree classifying the proteins according to their solubility (yes/no) has 35 final nodes and 65% overall accuracy in cross-validated tests. However, a number of the rules encoded within the tree were of much better predictive value. These are highlighted in Figure 1. Figure 1 depicts a decision tree for discriminating between soluble and insoluble proteins. The nodes of the tree are represented by ellipses (intermediate nodes) and rectangles (final nodes or leaves). The numbers on the left of each node denote the number of insoluble proteins in the

node, and are proportional to the node's dark area. Similarly, the numbers on the right denote the soluble proteins and are proportional to the white area. Under each intermediate node, the decision tree algorithm calculates all possible splitting thresholds for each of 53 variables (hydrophobicity, amino acid composition, etc.). It picks the optimal splitting variable and its threshold, in order for at least one of the two daughter nodes to be as homogeneous as possible. When a variable, v, is split, v≤threshold is the left branch, and v>threshold is the right branch. The specific parameters used at each node and their thresholds for the right branches shown in the graph are in descending order (from top root to bottom leaves): hydrophobe > 0.85 kcal/mole (where "hydrophobe" represents the average GES hydrophobicity of a sequence stretch, the higher this value the lower is the energy transfer); cplx>0.28 (a measure of a short complexity region based on the SEG program); Gln composition> 4%; Asp+Glu composition >17%; Ile-composition>5.6%; Phe+Tyr+Trp composition >7.5%; Asp+Glu composition > 13.6%; Gly+Ala+Val+Leu+Ile composition >42%; hydrophobe> 0.01 kcal/mole; His+Lys+Arg composition> 12%; Trp composition > 1.2%; and alpha-helical secondary structure composition > 58%. Note that two of the variables are conditioned on more than once (hydrophobe, Asp+Glu). The highlighted decision pathways terminate in highly homogeneous nodes (mostly dark is insoluble, mostly white is soluble). The shorter the decision pathway and the larger the number of cases in the terminal node, the less likely it is to over-fit the data. Heterogeneous leaves could be further split (dotted lines) improving the error rate but risking over-fitting of the training set. The usual technique for assessing the predictive success of rules suggested by the tree in the context of overfitting is cross-validation, where the overall data set is divided into test and training components. However, this technique is not optimal on the relatively small samples associated with each rule in these trees, as one has to leave out a substantial fraction of information in devising each rule. The predictive values of the highlighted decision pathways are evaluated using a "pessimistic estimation" procedure which assumes that the error rate at each node is bionomially distributed, and then inflates the rate found on a tree based on all the data (by ~2 standard deviations) to arrive at a more realistic estimate.

Proteins that fulfill the following sequence of four conditions are likely to be insoluble: (1) have a hydrophobic stretch - a long region (>20 residues) with average hydrophobicity less than -0.85 kcal/mole (on the GES scale,); (2) Gln composition <4%; (3) Asp+Glu composition <

17%; and (4) aromatic composition >7.5%. This rule has a 14% error rate in comparison to the default error rate of 39% for choosing a soluble protein without the aid of the tree. The probability that it could arise by chance is 1%, assuming one randomly chose the 24 insoluble proteins from the initial pool of 143 insoluble and 213 soluble proteins. These calculations are based on a "pessimistic estimate for errors"[11], taking the upper bound of the 95% confidence interval (see Fig. 3 for details). Conversely, proteins that do not have a hydrophobic stretch and have more than 27% of their residues in (hydrophilic) "low-complexity" regions are very likely to be soluble. This rule has a "pessimistic" error rate of 20% in contrast to 39% without the tree and a 1% probability of occurring by chance.

We also derived similar trees for expressability and crystallizability. We found that the composition of Asn appeared to be relevant to crystallizability. In particular, an Asn threshold of 3.5% was able to select a set of 18 crystallizable and only one non-crystallizable protein from our initial set of 25 crystallizable and 39 non-crystallizable proteins.

Together these data suggest that, using the database of protein sequence information, and biochemical and biophysical properties, it is possible to derive sets of "rules" from primary sequence that are predictive of a given protein's biophysical and biochemical properties.